Remarks

In view of the above amendments and the following remarks, reconsideration of the outstanding office action is respectfully requested.

This submission is accompanied by a Request for Continued Examination, a petition for extension of time, and an information disclosure statement. All fees should be withdrawn from Deposit Account 14-1138.

Claim 1 has been amended to recite higher stringency requirements (i.e., structural requirements of the claimed DNA molecule based on hybridization capability) as well the functional requirements of the encoded beta subunit ("form a beta clamp on a DNA strand"). The latter limitation finds descriptive support in the description present in the background of the invention at page 2, line 18 to page 3, line 31, and in Example 15. Claims 9 and 10 have been cancelled.

Claims 1, 2, 5-8, and 11-19 are pending. Claims 16-19 stand allowed.

The rejection of claims 1, 2, and 5-16 under 35 U.S.C. §112 (first paragraph) as lacking written descriptive support is respectfully traversed.

The PTO has asserted at page 3 of the outstanding office action that the "function" of the claimed beta subunit remains in question. (The office action recites "single-stranded binding proteins" at page 4, line 12, but elsewhere recites "beta subunit." Therefore, it is presumed that recitation of "single-stranded binding proteins" was an unintended error.) In any event, applicants respectfully disagree.

Claim 1 presently recites that "the isolated beta subunit can form a beta clamp on a DNA strand." Persons of skill in the art would appreciate that this is precisely the function attributed to beta subunits of polymerase III enzyme complexes. Indeed, in the prototypical polymerase III enzyme complex of *E. coli*, it is the function of the beta clamp (also known as sliding clamp) to bind to DNA and tether the polymerase subunit to the DNA being replicated. This leads to high processivity of the polymerase III enzyme complex as discussed at page 2, line 18, to page 3, line 31, of the present application.

That the isolated beta subunit presently claimed is structurally related to other beta subunits is evidenced by the comparison of the *Thermus thermophilus* (T.th.) beta subunit relative to other previously known beta subunits from *E. coli, P. mirabilis, H. influenzae, P. putida, and B. aphidicola* (see Figures 22A-B) and the comparison of the T.th. beta subunit of SEQ ID NO: 108 to the *B. stearothermophilus* beta subunit of SEQ ID NO:

174 (*see* page 61, lines 28-31). The latter two species show 21 percent identity over their length.

Even higher similarity among beta subunits would be expected among more closely related bacteria, and that is precisely what applicants demonstrated in the previous response (*see* Exhibits 1-3 attached to the August 22, 2006, amendment). Thus, given applicants prior demonstration of structural similarity among homologous beta subunits of *Bacillus*, applicants respectfully submit that the genus of isolated DNA being claimed is adequately represented by the species of SEQ ID NO: 174.

In view of all of the foregoing, applicants submit that the rejection of claims 1, 2, and 5-16 is improper and should be withdrawn.

The rejection of claims 1, 2, and 5-16 under 35 U.S.C. §112 (first paragraph) for lack of enablement is respectfully traversed.

It is the position of the PTO that the specification does not provide sufficient guidance for making and using other beta proteins within the scope of the claims. Applicants respectfully disagree.

The present application provides the nucleotide sequence of *Bacillus stearothermophilus dnaN* (e.g., SEQ ID NO: 173) and describes how one of ordinary skill can isolate homologs of the disclosed sequence (*see* page 41, line 9 to page 42, line 29; Example 12), express the beta subunit encoded by such homologous *dnaN* sequences (*see* Examples 12 and 22), and test the encoded beta subunit for activity (*see* Examples 26 and 30, using *Aquifex* beta subunit in assay). Thus, one of ordinary skill in the art would have been fully able to make and use DNA molecules and their encoded proteins within the scope of the presently claimed invention.

Moreover, with regard to method 3 for homolog identification, described at page 42, that is precisely the approach used to identify the *dnaN* homologs shown in Exhibit 1 of applicants' August 22, 2006, submission (i.e., from other *Bacillus* or *Geobacillus* organisms). For this reason, it should be apparent that the present application fully enables the production and use of other species of *Bacillus or Bacillus* (now *Geobacillus*) *stearothermophilus dnaN* homologs and their encoded beta subunits.

For these reasons, applicants submit that the rejection of claims 1, 2, and 5-16 for lack of enablement is improper and should be withdrawn.

In view of all of the foregoing, applicant submits that this case is in condition for allowance and such allowance is earnestly solicited.

Respectfully submitted,

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